

SEQUENCE LISTING

SEQ ID NO: 1

SEQUENCE LENGTH: 221

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Met Ala Pro Ala Arg Leu Phe Ala Leu Leu Phe Phe Val Gly Gly

1 5 10 15

Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu

20 25 30

Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val

35 40 45

Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly

50 55 60

Asp Leu Asp Asp Leu Glu Asp Ser Met Ile Gly Pro Glu Val Val His

65 70 75 80

Pro Leu Val Pro Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr

85 90 95

Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val

100 105 110

Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser

115 120 125

Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln

130 135 140

Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro

145 150 155 160

Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn

	165	170	175
Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu			
180	185	190	
Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln			
195	200	205	
Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp			
210	215	220	

SEQ ID NO: 2

SEQUENCE LENGTH: 663

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

SEQUENCE DESCRIPTION

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ATGGCCCCCG CCCGTCTGTT CGCGCTGCTG CTGTTCTTCG TAGGCGGAGT CGCCGAGTCG 60
ATCCGAGAGA CTGAGGTCAT CGACCCCCAG GACCTCCTAG AAGGCCGATA CTTCTCCGGA 120
GCCCTACCAG ACGATGAGGA TGTAGTGGGG CCCGGGCAGG AATCTGATGA CTTTGAGCTG 180
TCTGGCTCTG GAGATCTGGA TGACTTGGA GACTCCATGA TCGGCCCTGA AGTTGTCCAT 240
CCCTTGGTGC CTCTAGATGC TAATTACAAG AAGCCCAAAC TCCTCTACTG TAGCAACGGG 300
GGCCACTTCC TGAGGATCCT TCCGGATGGC ACAGTGGATG GGACAAGGGA CAGGAGCGAC 360
CAGCACATTC AGCTGCAGCT CAGTGCGGAA AGCGTGGGGG AGGTGTATAT AAAGAGTACC 420
GAGACTGGCC AGTACTTGGC CATGGACACC GACGGGCTTT TATACGGCTC ACAGACACCA 480
AATGAGGAAT GTTTGTTTCCT GGAAAGGCTG GAGGAGAACC ATTACAACAC CTATATATCC 540
AAGAAGCATG CAGAGAAGAA TTGGTTTGTT GGCCTCAAGA AGAATGGGAG CTGCAAACGC 600
GGTCCTCGGA CTCACTATGG CCAGAAAGCA ATCTTGTTTC TCCCCCTGCC AGTCTCTTCT 660
GAT

```

SEQ ID NO: 3

SEQUENCE LENGTH: 175

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val

5

10

15

Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala

20

25

30

Arg Ala Asn Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu

35

40

45

Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly

50

55

60

Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln

65

70

75

80

Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr

85

90

95

Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln

100

105

110

Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His

115

120

125

Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val

130

135

140

Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr

145

150

155

160

Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp

165

170

175

SEQ ID NO: 4

SEQUENCE LENGTH: 525

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

SEQUENCE DESCRIPTION

```
ATGTCCCGGG GAGCAGGACG TGTTCAGGGC ACGCTGCAGG CTCTCGTCTT CTTAGGCGTC 60
CTAGTGGGCA TGGTGGTGCC CTCACCTGCC GGCGCCCGCG CCAACGGCAC GCTACTGGAC 120
GCTAATTACA AGAAGCCCAA ACTCCTCTAC TGTAGCAACG GGGGCCACTT CCTGAGGATC 180
CTTCCGGATG GCACAGTGGA TGGGACAAGG GACAGGAGCG ACCAGCACAT TCAGCTGCAG 240
CTCAGTGCGG AAAGCGTGGG GGAGGTGTAT ATAAAGAGTA CCGAGACTGG CCAGTACTTG 300
GCCATGGACA CCGACGGGCT TTTATACGGC TCACAGACAC CAAATGAGGA ATGTTTGTTC 360
CTGGAAAGGC TGGAGGAGAA CCATTACAAC ACCTATATAT CCAAGAAGCA TGCAGAGAAG 420
AATTGGTTTG TTGGCCTCAA GAAGAATGGG AGCTGCAAAC GCGGTCCTCG GACTCACTAT 480
GGCCAGAAAG CAATCTTGTT TCTCCCCCTG CCAGTCTCTT CTGAT 525
```

SEQ ID NO: 5

SEQUENCE LENGTH: 181

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

```
Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
      5              10              15
Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
      20              25              30
Arg Ala Gln Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu
      35              40              45
Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly
```

50	55	60
Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln		
65	70	75
Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr		80
	85	90
Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln		95
100	105	110
Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Ala Ala		
115	120	125
Thr Pro Ala Pro Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala		
130	135	140
Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg		
145	150	155
Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu		160
	165	170
Pro Val Ser Ser Asp		175
180		

SEQ ID NO: 6

SEQUENCE LENGTH: 543

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

SEQUENCE DESCRIPTION

ATGTCCCGGG GAGCAGGACG TGTTCAAGGC ACGCTGCAGG CTCTCGTCTT CTTAGGCGTC 60
CTAGTGGGCA TGGTGGTGCC CTCACCTGCC GGCGCCCGCG CCCAAGGCAC GCTACTGGAC 120
GCTAATTACA AGAAGCCCAA ACTCCTCTAC TGTAAGCAACG GGGGCCACTT CCTGAGGATC 180
CTTCCGGATG GCACAGTGGA TGGGACAAGG GACAGGAGCG ACCAGCACAT TCAGCTGCAG 240

CTCAGTGC GG AAAGCGTGGG GGAGGTGTAT ATAAAGAGTA CCGAGACTGG CCAGTACTTG 300
 GCCATGGACA CCGACGGGCT TTTATACGGC TCACAGACAC CAAATGAGGA ATGTTTGTTC 360
 CTGGAAAGGC TGGAGGAGGC TGCTACTCCA GCTCCAAACC ATTACAACAC CTATATATCC 420
 AAGAAGCATG CAGAGAAGAA TTGGTTTGTG GGCCTCAAGA AGAATGGGAG CTGCAAACGC 480
 GGTCCCTCGGA CTCCTATGG CCAGAAAGCA ATCTTGTTTC TCCCCCTGCC AGTCTCTTCT 540
 GAT 543

SEQ ID NO: 7

SEQUENCE LENGTH: 30

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid synthetic DNA

SEQUENCE DESCRIPTION

TTGTCGACCC ACCATGGCCC CCGCCCGTCT 30

SEQ ID NO: 8

SEQUENCE LENGTH: 26

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid synthetic DNA

SEQUENCE DESCRIPTION

TTGATATCTA GAGGCACCAA GGGATG 26

SEQ ID NO: 9

SEQUENCE LENGTH: 35

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid synthetic DNA

SEQUENCE DESCRIPTION

GCGTCGACAG CGCTAATTAC AAGAAGCCCA AACTC

35

SEQ ID NO: 10

SEQUENCE LENGTH: 33

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid synthetic DNA

SEQUENCE DESCRIPTION

CCGAATTCTGA ATTCTTTAAT CAGAAGAGAC TGG

33

SEQ ID NO: 11

SEQUENCE LENGTH: 64

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid synthetic DNA

SEQUENCE DESCRIPTION

GCGTCGACCC ACCATGTCCC GGGGAGCAGG ACGTGTTTCTAG GGCACGCTGC AGGCTCTCGT

60

CTTC

64

SEQ ID NO: 12

SEQUENCE LENGTH: 29

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid synthetic DNA

SEQUENCE DESCRIPTION

GCGATATCCA GTAGCGTGCC GTTGGCGCG

29

SEQ ID NO: 13

SEQUENCE LENGTH: 18

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid synthetic DNA

SEQUENCE DESCRIPTION

GCGTCGACCC ACCATGTC

18

SEQ ID NO: 14

SEQUENCE LENGTH: 29

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid synthetic DNA

SEQUENCE DESCRIPTION

GCGATATCCA GTAGCGTGCC TTGGGCGCG

29

SEQ ID NO: 15

SEQUENCE LENGTH: 38

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid synthetic DNA

SEQUENCE DESCRIPTION

GCTGGAGGAG GCTGCTACTC CAGCTCCAAA CCATTACA

38

SEQ ID NO: 16

SEQUENCE LENGTH: 21

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid synthetic DNA

SEQUENCE DESCRIPTION

GCCGCTCTAG AACTAGTGGA T

21

SEQ ID NO: 17

SEQUENCE LENGTH: 200

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Met Ala Pro Ala Arg Leu Phe Ala Leu Leu Leu Phe Phe Val Gly Gly

1 5 10 15

Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu

20 25 30

Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val

35 40 45

Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly

50 55 60

Asp Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly

65 70 75 80

His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly Thr Arg Asp

85 90 95

Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu Ser Val Gly
 100 105 110
 Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu Ala Met Asp
 115 120 125
 Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu Glu Cys Leu
 130 135 140
 Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser Lys
 145 150 155 160
 Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser
 165 170 175
 Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe
 180 185 190
 Leu Pro Leu Pro Val Ser Ser Asp
 195 200

SEQ ID NO: 18

SEQUENCE LENGTH: 600

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

SEQUENCE DESCRIPTION

ATGGCCCCCG CCCGTCTGTT CGCGCTGCTG CTGTTCTTCG TAGGCGGAGT CGCCGAGTCG 60
 ATCCGAGAGA CTGAGGTCAT CGACCCCCAG GACCTCCTAG AAGGCCGATA CTTCTCCGGA 120
 GCCCTACCAG ACGATGAGGA TGTAGTGGGG CCCGGGCAGG AATCTGATGA CTTTGAGCTG 180
 TCTGGCTCTG GAGATGCTAA TTACAAGAAG CCCAAACTCC TCTACTGTAG CAACGGGGGC 240
 CACTTCCTGA GGATCCTTCC GGATGGCACA GTGGATGGGA CAAGGGACAG GAGCGACCAG 300
 CACATTCAGC TGCAGCTCAG TGCGGAAAGC GTGGGGGAGG TGTATATAAA GAGTACCGAG 360
 ACTGGCCAGT ACTTGGCCAT GGACACCGAC GGGCTTTTAT ACGGCTCACA GACACCAAAT 420

GAGGAATGTT TGTTCTGGA AAGGCTGGAG GAGAACCATT ACAACACCTA TATATCCAAG 480
AAGCATGCAG AGAAGAATTG GTTTGTTGGC CTCAAGAAGA ATGGGAGCTG CAAACGCGGT 540
CCTCGGACTC ACTATGGCCA GAAAGCAATC TTGTTTCTCC CCCTGCCAGT CTCTTCTGAT 600

SEQ ID NO: 19

SEQUENCE LENGTH: 200

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Met Ala Pro Ala Arg Leu Phe Ala Leu Leu Leu Phe Phe Val Gly Gly
5 10 15
Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu
20 25 30
Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Ser Asp Asp Glu Asp Val
35 40 45
Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly
50 55 60
Asp Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly
65 70 75 80
His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly Thr Arg Asp
85 90 95
Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu Ser Val Gly
100 105 110
Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu Ala Met Asp
115 120 125
Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu Glu Cys Leu
130 135 140
Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser Lys

145 150 155 160
 Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser
 165 170 175
 Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe
 180 185 190
 Leu Pro Leu Pro Val Ser Ser Asp
 195 200

SEQ ID NO: 20

SEQUENCE LENGTH: 600

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

SEQUENCE DESCRIPTION

ATGGCCCCCG CCGTCTGTT CGCGCTGCTG CTGTTCTTCG TAGGCGGAGT CGCCGAGTCG 60
 ATCCGAGAGA CTGAGGTCAT CGACCCCCAG GACCTCCTAG AAGGCCGATA CTTCTCCGGA 120
 GCCCTATCAG ACGATGAGGA TGTAGTGGGG CCCGGGCAGG AATCTGATGA CTTTGAGCTG 180
 TCTGGCTCTG GAGATGCTAA TTACAAGAAG CCCAAACTCC TCTACTGTAG CAACGGGGGC 240
 CACTTCCTGA GGATCCTTCC GGATGGCACA GTGGATGGGA CAAGGGACAG GAGCGACCAG 300
 CACATTCAGC TGCAGCTCAG TGCAGAAAGC GTGGGGGAGG TGTATATAAA GAGTACCGAG 360
 ACTGGCCAGT ACTTGGCCAT GGACACCGAC GGGCTTTTAT ACGGCTCACA GACACCAAAT 420
 GAGGAATGTT TGTTCTGGA AAGGCTGGAG GAGAACCATT ACAACACCTA TATATCCAAG 480
 AAGCATGCAG AGAAGAATTG GTTTGTTGGC CTCAAGAAGA ATGGGAGCTG CAAACGCGGT 540
 CCTCGGACTC ACTATGGCCA GAAAGCAATC TTGTTTCTCC CCCTGCCAGT CTCTTCTGAT 600

SEQ ID NO: 21

SEQUENCE LENGTH: 254

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Met Ala Pro Ala Arg Leu Phe Ala Leu Leu Leu Phe Phe Val Gly Gly
5 10 15
Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu
20 25 30
Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val
35 40 45
Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly
50 55 60
Asp Leu Asp Asp Leu Glu Asp Ser Met Ile Gly Pro Glu Val Val His
65 70 75 80
Pro Leu Val Pro Leu Asp Asn His Ile Pro Glu Arg Ala Gly Ser Gly
85 90 95
Ser Gln Val Pro Thr Glu Pro Lys Lys Leu Glu Glu Asn Glu Val Ile
100 105 110
Pro Lys Arg Ile Ser Pro Val Ala Asn Tyr Lys Lys Pro Lys Leu Leu
115 120 125
Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr
130 135 140
Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu
145 150 155 160
Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly
165 170 175
Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr
180 185 190
Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr
195 200 205

Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly
 210 215 220
 Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly
 225 230 235 240
 Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
 245 250

SEQ ID NO: 22

SEQUENCE LENGTH: 762

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

SEQUENCE DESCRIPTION

ATGGCCCCCG	CCCGTCTGTT	CGCGCTGCTG	CTGTTCTTCG	TAGGCGGAGT	CGCCGAGTCG	60
ATCCGAGAGA	CTGAGGTCAT	CGACCCCCAG	GACCTCCTAG	AAGGCCGATA	CTTCTCCGGA	120
GCCCTACCAG	ACGATGAGGA	TGTAGTGGGG	CCCGGGCAGG	AATCTGATGA	CTTTGAGCTG	180
TCTGGCTCTG	GAGATCTGGA	TGACTTGGA	GACTCCATGA	TCGGCCCTGA	AGTTGTCCAT	240
CCCTTGGTGC	CTCTAGATAA	CCATATCCCT	GAGAGGGCAG	GGTCTGGGAG	CCAAGTCCCC	300
ACCGAACCCA	AGAAACTAGA	GGAGAATGAG	GTTATCCCCA	AGAGAATCTC	ACCCGTTGCT	360
AATTACAAGA	AGCCCAAAC	CCTCTACTGT	AGCAACGGGG	GCCACTTCCT	GAGGATCCTT	420
CCGGATGGCA	CAGTGGATGG	GACAAGGGAC	AGGAGCGACC	AGCACATTCA	GCTGCAGCTC	480
AGTGCGGAAA	GCGTGGGGGA	GGTGTATATA	AAGAGTACCG	AGACTGGCCA	GTA CT TGGCC	540
ATGGACACCG	ACGGGCTTTT	ATACGGCTCA	CAGACACCAA	ATGAGGAATG	TTTGTTCTCTG	600
GAAAGGCTGG	AGGAGAACCA	TTACAACACC	TATATATCCA	AGAAGCATGC	AGAGAAGAAT	660
TGGTTTGTTG	GCCTCAAGAA	GAATGGGAGC	TGCAAACGCG	GTCCTCGGAC	TCACTATGGC	720
CAGAAAGCAA	TCTTGTTTCT	CCCCCTGCCA	GTCTCTTCTG	AT		762

SEQ ID NO: 23

SEQUENCE LENGTH: 281

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Met Ala Pro Ala Arg Leu Phe Ala Leu Leu Leu Phe Phe Val Gly Gly
5 10 15
Val Ala Glu Ser Ile Arg Glu Thr Glu Val Ile Asp Pro Gln Asp Leu
20 25 30
Leu Glu Gly Arg Tyr Phe Ser Gly Ala Leu Pro Asp Asp Glu Asp Val
35 40 45
Val Gly Pro Gly Gln Glu Ser Asp Asp Phe Glu Leu Ser Gly Ser Gly
50 55 60
Asp Leu Asp Asp Leu Glu Asp Ser Met Ile Gly Pro Glu Val Val His
65 70 75 80
Pro Leu Val Pro Leu Asp Asn His Ile Pro Glu Arg Ala Gly Ser Gly
85 90 95
Ser Gln Val Pro Thr Glu Pro Lys Lys Leu Glu Glu Asn Glu Val Ile
100 105 110
Pro Lys Arg Ile Ser Pro Val Glu Glu Ser Glu Asp Val Ser Asn Lys
115 120 125
Val Ser Met Ser Ser Thr Val Gln Gly Ser Asn Ile Phe Glu Arg Thr
130 135 140
Glu Val Ala Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser Asn Gly
145 150 155 160
Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly Thr Arg
165 170 175
Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu Ser Val
180 185 190

Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu Ala Met
 195 200 205
 Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu Glu Cys
 210 215 220
 Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr Ile Ser
 225 230 235 240
 Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly
 245 250 255
 Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu
 260 265 270
 Phe Leu Pro Leu Pro Val Ser Ser Asp
 275 280

SEQ ID NO: 24

SEQUENCE LENGTH: 843

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

SEQUENCE DESCRIPTION

ATGGCCCCCG CCCGTCTGTT CGCGCTGCTG CTGTTCTTCG TAGGCGGAGT CGCCGAGTCG 60
 ATCCGAGAGA CTGAGGTCAT CGACCCCCAG GACCTCCTAG AAGGCCGATA CTTCTCCGGA 120
 GCCCTACCAG ACGATGAGGA TGTAGTGGGG CCCGGGCAGG AATCTGATGA CTTTGAGCTG 180
 TCTGGCTCTG GAGATCTGGA TGA CTGGAA GACTCCATGA TCGGCCCTGA AGTTGTCCAT 240
 CCCTTGGTGC CTCTAGATAA CCATATCCCT GAGAGGGCAG GGTCTGGGAG CCAAGTCCCC 300
 ACCGAACCCA AGAAACTAGA GGAGAATGAG GTTATCCCCA AGAGAATCTC ACCCGTTGAA 360
 GAGAGTGAGG ATGTGTCCAA CAAGGTGTCA ATGTCCAGCA CTGTGCAGGG CAGCAACATC 420
 TTTGAGAGAA CGGAGGTCGC TAATTACAAG AAGCCCCAAC TCCTCTACTG TAGCAACGGG 480
 GGCCACTTCC TGAGGATCCT TCCGGATGGC ACAGTGGATG GGACAAGGGA CAGGAGCGAC 540

Tyr Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys
 130 135 140
 Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys
 145 150 155 160
 Ala Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
 165 170

SEQ ID NO: 26

SEQUENCE LENGTH: 516

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

SEQUENCE DESCRIPTION

ATGTCCCGGG GAGCAGGACG TGTTCAAGGC ACGCTGCAGG CTCTCGTCTT CTTAGGCGTC 60
 CTAGTGGGCA TGGTGGTGCC CTCACCTGCC GGCGCCCGCG CCAACGGCTC GGCTAATTAC 120
 AAGAAGCCCA AACTCCTCTA CTGTAGCAAC GGGGGCCACT TCCTGAGGAT CCTTCCGGAT 180
 GGCACAGTGG ATGGGACAAG GGACAGGAGC GACCAGCACA TTCAGCTGCA GCTCAGTGCG 240
 GAAAGCGTGG GGGAGGTGTA TATAAAGAGT ACCGAGACTG GCCAGTACTT GGCCATGGAC 300
 ACCGACGGGC TTTTATACGG CTCACAGACA CCAAATGAGG AATGTTTGTT CCTGGAAAGG 360
 CTGGAGGAGA ACCATTACAA CACCTATATA TCCAAGAAGC ATGCAGAGAA GAATTGGTTT 420
 GTTGGCCTCA AGAAGAATGG GAGCTGCAAA CGCGGTCCTC GGACTCACTA TGGCCAGAAA 480
 GCAATCTTGT TTCTCCCCTT GCCAGTCTCT TCTGAT 516

SEQ ID NO: 27

SEQUENCE LENGTH: 210

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val
5 10 15

Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala
20 25 30

Arg Ala Asn Gly Thr Leu Leu Asp Ser Arg Gly Trp Gly Thr Leu Leu
35 40 45

Ser Arg Ser Arg Ala Gly Leu Ala Gly Glu Ile Ser Gly Val Asn Trp
50 55 60

Glu Ser Gly Tyr Leu Val Gly Ile Lys Arg Gln Ala Asn Tyr Lys Lys
65 70 75 80

Pro Lys Leu Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu
85 90 95

Pro Asp Gly Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile
100 105 110

Gln Leu Gln Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser
115 120 125

Thr Glu Thr Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr
130 135 140

Gly Ser Gln Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu
145 150 155 160

Glu Asn His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu Lys Asn
165 170 175

Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly Pro Arg
180 185 190

Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro Val Ser
195 200 205

Ser Asp
210

SEQ ID NO: 28

SEQUENCE LENGTH: 630

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

SEQUENCE DESCRIPTION

ATGTCCCGGG	GAGCAGGACG	TGTTTCAGGGC	ACGCTGCAGG	CTCTCGTCTT	CTTAGGCGTC	60
CTAGTGGGCA	TGGTGGTGCC	CTCACCTGCC	GGCGCCCGCG	CCAACGGCAC	GCTACTGGAC	120
TCCAGAGGCT	GGGGCACCCCT	CTTGTCCAGG	TCTCGAGCTG	GGCTAGCTGG	AGAGATTTCG	180
GGTGTGAATT	GGGAAAGCGG	CTATTTGGTG	GGCATTAAAGC	GACAGGCTAA	TTACAAGAAG	240
CCCAAACCTCC	TCTACTGTAG	CAACGGGGGC	CACTTCCTGA	GGATCCTTCC	GGATGGCACA	300
GTGGATGGGA	CAAGGGACAG	GAGCGACCAG	CACATTCAGC	TGCAGCTCAG	TGCGGAAAGC	360
GTGGGGGAGG	TGTATATAAA	GAGTACCGAG	ACTGGCCAGT	ACTTGCCCAT	GGACACCGAC	420
GGGCTTTTAT	ACGGCTCACA	GACACCAAAT	GAGGAATGTT	TGTTCCCTGGA	AAGGCTGGAG	480
GAGAACCATT	ACAACACCTA	TATATCCAAG	AAGCATGCAG	AGAAGAATTG	GTTTGTGGC	540
CTCAAGAAGA	ATGGGAGCTG	CAAACGCGGT	CCTCGGACTC	ACTATGGCCA	GAAAGCAATC	600
TTGTTTCTCC	CCCTGCCAGT	CTCTTCTGAT				630

SEQ ID NO: 29

SEQUENCE LENGTH: 180

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION

Met Ser Arg Gly Ala Gly Arg Val Gln Gly Thr Leu Gln Ala Leu Val

5

10

15

Phe Leu Gly Val Leu Val Gly Met Val Val Pro Ser Pro Ala Gly Ala

20	25	30
Arg Ala Asn Gly Thr Leu Leu Asp Ala Asn Tyr Lys Lys Pro Lys Leu		
35	40	45
Leu Tyr Cys Ser Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly		
50	55	60
Thr Val Asp Gly Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln		
65	70	75
Leu Ser Ala Glu Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr		
85	90	95
Gly Gln Tyr Leu Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln		
100	105	110
Thr Pro Asn Glu Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn Ala		
115	120	125
Thr Pro Ala Pro His Tyr Asn Thr Tyr Ile Ser Lys Lys His Ala Glu		
130	135	140
Lys Asn Trp Phe Val Gly Leu Lys Lys Asn Gly Ser Cys Lys Arg Gly		
145	150	155
Pro Arg Thr His Tyr Gly Gln Lys Ala Ile Leu Phe Leu Pro Leu Pro		
165	170	175
Val Ser Ser Asp		
180		

SEQ ID NO: 30

SEQUENCE LENGTH: 540

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

SEQUENCE DESCRIPTION

ATGTCCCGGG	GAGCAGGACG	TGTTTCAGGGC	ACGCTGCAGG	CTCTCGTCTT	CTTAGGCGTC	60
CTAGTGGGCA	TGGTGGTGCC	CTCACCTGCC	GGCGCCCGCG	CCAACGGCAC	GCTACTGGAC	120
GCTAATTACA	AGAAGCCCAA	ACTCCTCTAC	TGTAGCAACG	GGGGCCACTT	CCTGAGGATC	180
CTTCCGGATG	GCACAGTGGA	TGGGACAAGG	GACAGGAGCG	ACCAGCACAT	TCAGCTGCAG	240
CTCAGTGCGG	AAAGCGTGGG	GGAGGTGTAT	ATAAAGAGTA	CCGAGACTGG	CCAGTACTTG	300
GCCATGGACA	CCGACGGGCT	TTTATACGGC	TCACAGACAC	CAAATGAGGA	ATGTTTGTTT	360
CTGGAAAGGC	TGGAGGAGAA	CGCTACTCCA	GCTCCACATT	ACAACACCTA	TATATCCAAG	420
AAGCATGCAG	AGAAGAATTG	GTTTGTTGGC	CTCAAGAAGA	ATGGGAGCTG	CAAACGCGGT	480
CCTCGGACTC	ACTATGGCCA	GAAAGCAATC	TTGTTTCTCC	CCCTGCCAGT	CTCTTCTGAT	540